IN THE CLAIMS:

Please amend the claims to read as follows:

1.-121. (Cancelled)

122. (Currently Amended) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons ~~73,~~55, ~~48, 20,~~ 43, 53, ~~90,~~13, ~~84,~~23, 33, 74, 32, 39, 60, ~~36,~~and 35, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 54, ~~84, 82,~~ 46, 13, 74, 55, 85, ~~20, 72,~~ 62, 66, ~~84, 48,~~ 33, ~~73, 71,~~ 64, 93, 23, and 58, ~~and 36,~~ wherein the presence of said protease-encoding nucleic acid in said biological sample in comparison indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease.

123. (Previously Pending) The method of Claim 122, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) or said mutation at codon 90 is a substitution of methionine (M) for leucine (L).

124. (Currently Amended) The method of Claim 122, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons ~~73,~~55, ~~48, 20,~~ 43, 53, ~~90,~~13, 23, ~~84, 53,~~ 74, 60, 33, ~~36,~~35, and 32, ~~and 46,~~ or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, 54, ~~82,~~ 85, ~~84, 20, 72,~~ 62, 74, 53, ~~48,~~ 23, 58, ~~36,~~ 64, 77, and 93.

125. (Previously Pending) The method of claim 124, wherein said difference in said HIV's susceptibility to amprenavir relative to a reference HIV is greater than 10 fold.

126. (Currently Amended) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 33, 23, ~~84,~~32, 53, ~~90,~~37, 71, ~~10, 54,~~ 61, 11, and

46, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 89, 53, ~~84,~~ 33, 92, 95, 54, 58, 46, ~~82, 36, 10,~~ 62, 74, 15, 47, 66, 32, 55, 53, 13, and 69, wherein the presence of said protease-encoding nucleic acid in said biological sample in comparison indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease.

127. (Currently Amended) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons ~~73,~~ 55, 53, 23, 33, and 39, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 55, 85, 66, 33, ~~73,~~ 23, and 58, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease.

128. (Previously Pending) The method of Claim 127, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) or said mutation at codon 90 is a substitution of methionine (M) for leucine (L).

129. (Previously Pending) The method of Claim 127, wherein said protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

130. (Currently Amended) The method of Claim 129, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, ~~73,~~ 53, 33, and 39, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 66, and 33, ~~and~~ ~~73,~~ and wherein said protease inhibitor is saquinavir.

131. (Currently Amended) The method of Claim 130, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, ~~73,~~ 53, and 33, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 66, and 33, ~~and~~ ~~73,~~ and wherein said difference in said HIV protease's susceptibility to a protease

inhibitor relative to a reference HIV protease is a decrease in susceptibility to saquinavir.

132. (Currently Amended) The method of Claim 129, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53 and 95, ~~, 95, and 46,~~ and wherein said protease inhibitor is indinavir.

133. (Currently Amended) The method of Claim 132, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53 and 95, ~~, 95, and 46,~~ and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to indinavir.

134. (Currently Amended) The method of Claim 129, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons ~~73,~~ 55, 53, 23, and 33, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, 85, 53, 23, 58, and 77.

135. (Previously Pending) The method of claim 127, wherein said difference in said HIV protease's susceptibility to said protease inhibitor relative to a reference HIV is greater than 10 fold.

136. (Previously Pending) The method of claim 128, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, 53, 33, and 35, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 23, and 58, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to saquinavir.

137. (Currently Amended) The method of claim 128, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons ~~73, 55,~~ 55 and 53, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, and 85, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to indinavir.

138. (Previously Pending) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 33, 23, 53, and 11, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 89, 53, 33, 92, 95, 58, 66, and 55, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a ~~difference~~ decrease in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease.

139. (Currently Amended) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 32 and 46; the group consisting of codons 13 and 61; or the group consisting of codons 32 and 39, ~~73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35~~, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 64, 77, and 93; the group consisting of codons 13 and 74; or the group consisting of codons 74, 15, and 69, ~~53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71, 64, 93, 23, 58, and 36~~, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates an increase in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease.

140. (Previously Pending) The method of Claim 139, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) or said mutation at codon 90 is a substitution of methionine (M) for leucine (L).

141. (Previously Pending) The method of Claim 139, wherein said protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

142. (Cancelled)

143. (Currently Amended) The method of Claim 141, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at codon 32 or codon 39, or a

mutation at codon 90 and a secondary mutation at codon 64 or codon 93, and wherein said protease inhibitor is saquinavir.

144. (Cancelled)

145. (Currently Amended) The method of Claim 141, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at codon 13, or a mutation at codon 90 and a secondary mutation at codon 13 or codon 74, and wherein said protease inhibitor is indinavir.

146. (Cancelled)

147. (Previously Pending) The method of claim 139, wherein said increase in said HIV protease's susceptibility to said protease inhibitor relative to a reference HIV protease is greater than 10 fold.

148. (Previously Pending) The method of claim 139, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codon 32 or codon 46, or a mutation at codon 90 and a secondary mutation at codon 64, codon 77, or codon 93, and wherein said protease inhibitor is saquinavir.

149. (Cancelled)

150. (Currently Amended) A test vector, comprising:

(a) a segment derived from HIV from an HIV-infected patient, which segment comprises a protease-encoding nucleic acid, wherein said protease-encoding nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons ~~73,~~55, 53, 23, 33, and 39, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 55, 85, 66, 33, ~~73,~~23, and 58; and

(b) an indicator gene, wherein the amount of expression of said indicator gene in a host cell depends upon the activity of said HIV protease.